

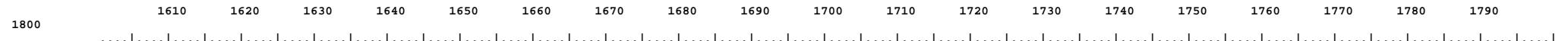
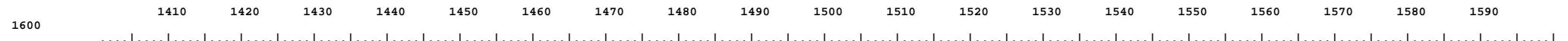
This figure displays a sequence alignment of various proteins across 190 positions. The alignment is color-coded to represent different amino acid residues at each position, allowing for the comparison of conservation and divergence across the dataset. The x-axis represents the position from 10 to 190, and the y-axis lists the protein identifiers.

Key features of the alignment include:

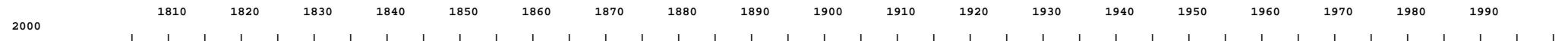
- Color Coding:** Amino acids are represented by specific colors: Red, Green, Blue, Yellow, Magenta, Cyan, and Black.
- Conservation:** Positions where most proteins share the same color are considered conserved.
- Divergence:** Positions showing significant variation in color across the proteins are considered divergent.
- Protein Identifiers:** The y-axis lists numerous protein identifiers, including 24584954.f, 24640167.f, 6753370.m, 34875877.m, cdc7.h, 19173519.y, 19074621.y, 6320187.y, 39942816.y, 32423105.y, 19113120.y, 19113119.y, 19113390.y, 17505857.w, 2phr\_PHK, 113r\_PKA, 23508418.z, 23593305.z, 2erk\_Erk2, 1jwh\_CKII, 23508651.z, lias\_TGFbr, and 400 additional entries starting from 210.



34875877.m  
CDC7.h  
19173519.y  
19074621.y  
6320187.y  
39942816.y  
3242857.y **EAIINIMDAVSNVIAEIKYTDILKRAKLSIGMYQYRFHQKLTOENKVMAVQLQRVVEALGVVYLKTLDKAALGKADQEGIVLDTSLLLKGADQINLYKLIRYVESKLAFKIEGYISYCREEGRDIDDEAAETEIKAQGRPPVLTTLCSFLTALTNLSSGRIFYEKIPPRGELODMKLSYMLLSPTHAFSSIAES**  
19113120.y  
19113119.y  
19113390.y  
17505857.w  
2phk\_PHK  
113r\_PKA  
23508418.z  
23593305.z  
2erk\_Erk2  
1jwh\_CKII  
32508651.z **YNHYNYITYLKKNKHMNDKTNGDMKNVQNKCSONIRDTEDFIHYNQKKSSSLFLYDIDNMKKILKNYKKQMDTKEVLAKTTFKMSDLISKKYKEQKCICKKDITFTRDIVINPMLNNRNLDLNNEKVENKEEKKINDSTYVKEEGKKCRDIKKIEHIYNYDCDKMNNEHNEYVTHYKKDRINVLSGKNINVVEDINFRWH**  
1lias\_TGFBR



24584954.f  
24640167.f  
6753370.m  
34875877.m  
CDC7.h  
19173519.y  
19074621.y  
6320187.y  
39942816.y  
32423105.v  
VGMPYINPHSPWILARREYLEANFIKRYTASQQTSTATAPLFAPVIPPPSNITHYSINPSSSRNKKDHKPANVRKLAARDSHOFYENATLRAVNQSIGRAIRHQNDYAAIVLIDNRFEKEHVRAKLPGWIREGWDETQRQA  
KEDGKALKGLQGMGRVNMFGRGNVMLVCRGHVVVEYNGYSTFDRMNCHGTHVSJDQAA  
19113120.y  
19113119.y  
19113390.y  
19113587.w  
17505857.w  
2phk\_PHK  
113r\_PKA  
23508418.z  
23593305.z  
2erk\_Erk2  
1jwh\_CKII  
NDSCINSSYGSTYKNEDHKIELRHNPDLTKE TDLS TSDKKFNFKNKTTYDCLKHNNLNISTGKRRDLYKNDL INILNEKEBQVGDVLKGEDSYKQIDKKVDVBIYRKEKNSLDI SNNIIIINFMNNTYHHKNNSIEKRTDTPMKYYMDTLNYFDNKNM  
LDHKDKEVKVLMMGNDKKSGLNYYDMTNDDKEDTCTKMF  
lias\_TGFBR



24584954.f  
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6320187.y  
39942816.y  
32423105.y RTCR

